

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: BASF Aktiengesellschaft
- (B) STREET: Carl-Bosch-Strasse 38
- (C) CITY: Ludwigshafen
- (E) COUNTRY: Federal Republic of Germany
- (F) POSTAL CODE: D-67056
- (G) TELEPHONE: 0621/6048526
- (H) TELEFAX: 0621/6043123
- (I) TELEX: 1762175170

(ii) TITLE OF APPLICATION: Genes of purine biosynthesis from *Ashbya gossypii* and their use in microbial riboflavin biosynthesis

(iii) NUMBER OF SEQUENCES: 13

## (iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1911 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

## (ix) FEATURES:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..625

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 626..1582

## (ix) FEATURES:

- (A) NAME/KEY: 3'UTR

(B) LOCATION: 1583..1911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGTAGTCGCT CATCGACAGA CACAATCGCG TGTTCTCTCT GAATCGTCCA TTGGGTGTCA 60

GCATCCTGAT CGCGGGCGGA TGGAATGGGT AATCATTAGG AAACACCAAT GTCCCATGGT 120

ATTGTCCGTC CTCGTATGGT GTCTCAGGAG GACCCGTGAT CACGTAGTGC CACACCAGGA 180

TATTGTCTTC CTTTGGTGCT GCCACGATGT AGGGCGGGGG GTTCTCGGTC ATCATTTTGT 240

ACTCCTTTGA GAGCCGCTTG TACGCCTGTC TTGATGCCAT CTTGCCTACT ATTAGTTTCT 300

CACCACTTCC CGCCAAACAA TCTGCACTTT ACGAGCGCTA TCTATCCCTC GGGTCGCTCT 360

AGTTGATTAT TGGCGAACT GATAGTTCAG GTACTTCCAT GATGCGGTCA TATCCACGTA 420

TGTGATCAG TGATCATCAG CCATGCTGCC AGCTCACGGG CCTGCCTACA CTATTGGAGG 480

CTCTGTGAGT CATGATTTAT TGCATATCAA GCCCAGATAG TCGTTGGGGA TACTACCGTT 540

GCCGCGATGA GCTCCGATAT TAAGTTGTAG CCAAAAATTT TAACGGATGA CTTCTTAACA 600

GTTATTGACG CCGCAATCCT ACGCC ATG TCG TCC AAT AGC ATA AAG CTG CTA 652  
Met Ser Ser Asn Ser Ile Lys Leu Leu  
1 5

GCA GGT AAC TCG CAC CCG GAC CTA GCT GAG AAG GTC TCC GTT CGC CTA 700  
Ala Gly Asn Ser His Pro Asp Leu Ala Glu Lys Val Ser Val Arg Leu  
10 15 20 25

GGT GTA CCA CTT TCG AAG ATT GGA GTG TAT CAC TAC TCT AAC AAA GAG 748  
Gly Val Pro Leu Ser Lys Ile Gly Val Tyr His Tyr Ser Asn Lys Glu  
30 35 40

ACG TCA GTT ACT ATC GGC GAA AGT ATC CGT GAT GAA GAT GTC TAC ATC 796  
Thr Ser Val Thr Ile Gly Glu Ser Ile Arg Asp Glu Asp Val Tyr Ile  
45 50 55

ATC CAG ACA GGA ACG GGG GAG CAG GAA ATC AAC GAC TTC CTC ATG GAA 844  
Ile Gln Thr Gly Thr Gly Glu Gln Glu Ile Asn Asp Phe Leu Met Glu  
60 65 70

CTG CTC ATC ATG ATC CAT GCC TGC CGG TCA GCC TCT GCG CGG AAG ATC 892  
Leu Leu Ile Met Ile His Ala Cys Arg Ser Ala Ser Ala Arg Lys Ile  
75 80 85

205T20.15T20.1024502

ACA GCG GTT ATA CCA AAC TTC CCT TAC GCA AGA CAA GAC AAA AAG GAC	940
Thr Ala Val Ile Pro Asn Phe Pro Tyr Ala Arg Gln Asp Lys Lys Asp	
90 95 100 105	
AAG TCG CGA GCA CCG ATA ACT GCC AAG CTG GTG GCC AAG ATG CTA GAG	988
Lys Ser Arg Ala Pro Ile Thr Ala Lys Leu Val Ala Lys Met Leu Glu	
110 115 120	
ACC GCG GGG TGC AAC CAC GTT ATC ACG ATG GAT TTG CAC GCG TCT CAA	1036
Thr Ala Gly Cys Asn His Val Ile Thr Met Asp Leu His Ala Ser Gln	
125 130 135	
ATT CAG GGT TTC TTC CAC ATT CCA GTG GAC AAC CTA TAT GCA GAG CCG	1084
Ile Gln Gly Phe Phe His Ile Pro Val Asp Asn Leu Tyr Ala Glu Pro	
140 145 150	
AAC ATC CTG CAC TAC ATC CAA CAT AAT GTG GAC TTC CAG AAT AGT ATG	1132
Asn Ile Leu His Tyr Ile Gln His Asn Val Asp Phe Gln Asn Ser Met	
155 160 165	
TTG GTC GCG CCA GAC GCG GGG TCG GCG AAG CGC ACG TCG ACG CTT TCG	1180
Leu Val Ala Pro Asp Ala Gly Ser Ala Lys Arg Thr Ser Thr Leu Ser	
170 175 180 185	
GAC AAG CTG AAT CTC AAC TTC GCG TTG ATC CAC AAA GAA CGG CAG AAG	1228
Asp Lys Leu Asn Leu Asn Phe Ala Leu Ile His Lys Glu Arg Gln Lys	
190 195 200	
GCG AAC GAG GTC TCG CGG ATG GTG TTG GTG GGT GAT GTC GCC GAC AAG	1276
Ala Asn Glu Val Ser Arg Met Val Leu Val Gly Asp Val Ala Asp Lys	
205 210 215	
TCC TGT ATT ATT GTA GAC GAC ATG GCG GAC ACG TGC GGA ACG CTA GTG	1324
Ser Cys Ile Ile Val Asp Asp Met Ala Asp Thr Cys Gly Thr Leu Val	
220 225 230	
AAG GCC ACT GAC ACG CTG ATC GAA AAT TGT GCG AAA GAA GTG ATT GCC	1372
Lys Ala Thr Asp Thr Leu Ile Glu Asn Cys Ala Lys Glu Val Ile Ala	
235 240 245	
ATT GTG ACA CAC GGT ATA TTT TCT GGC GGC GCC CGC GAG AAG TTG CGC	1420
Ile Val Thr His Gly Ile Phe Ser Gly Gly Ala Arg Glu Lys Leu Arg	
250 255 260 265	
AAC AGC AAG CTG GCA CGG ATC GTA AGC ACA AAT ACG GTG CCA GTG GAC	1468
Asn Ser Lys Leu Ala Arg Ile Val Ser Thr Asn Thr Val Pro Val Asp	
270 275 280	

20576157 021502

(2) INFORMATION FOR SEQ ID NO: 2:

(A) LENGTH: 318 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ser	Ser	Asn	Ser	Ile	Lys	Leu	Leu	Ala	Gly	Asn	Ser	His	Pro	Asp
1				5					10					15	
Leu	Ala	Glu	Lys	Val	Ser	Val	Arg	Leu	Gly	Val	Pro	Leu	Ser	Lys	Ile
			20					25					30		
Gly	Val	Tyr	His	Tyr	Ser	Asn	Lys	Glu	Thr	Ser	Val	Thr	Ile	Gly	Glu
		35					40					45			
Ser	Ile	Arg	Asp	Glu	Asp	Val	Tyr	Ile	Ile	Gln	Thr	Gly	Thr	Gly	Glu
	50					55					60				
Gln	Glu	Ile	Asn	Asp	Phe	Leu	Met	Glu	Leu	Leu	Ile	Met	Ile	His	Ala
65					70					75					80

Cys Arg Ser Ala Ser Ala Arg Lys Ile Thr Ala Val Ile Pro Asn Phe  
                                     85                                    90                                    95  
 Pro Tyr Ala Arg Gln Asp Lys Lys Asp Lys Ser Arg Ala Pro Ile Thr  
                                     100                                    105                                    110  
 Ala Lys Leu Val Ala Lys Met Leu Glu Thr Ala Gly Cys Asn His Val  
                                     115                                    120                                    125  
 Ile Thr Met Asp Leu His Ala Ser Gln Ile Gln Gly Phe Phe His Ile  
                                     130                                    135                                    140  
 Pro Val Asp Asn Leu Tyr Ala Glu Pro Asn Ile Leu His Tyr Ile Gln  
                                     145                                    150                                    155                                    160  
 His Asn Val Asp Phe Gln Asn Ser Met Leu Val Ala Pro Asp Ala Gly  
                                     165                                    170                                    175  
 Ser Ala Lys Arg Thr Ser Thr Leu Ser Asp Lys Leu Asn Leu Asn Phe  
                                     180                                    185                                    190  
 Ala Leu Ile His Lys Glu Arg Gln Lys Ala Asn Glu Val Ser Arg Met  
                                     195                                    200                                    205  
 Val Leu Val Gly Asp Val Ala Asp Lys Ser Cys Ile Ile Val Asp Asp  
                                     210                                    215                                    220  
 Met Ala Asp Thr Cys Gly Thr Leu Val Lys Ala Thr Asp Thr Leu Ile  
                                     225                                    230                                    235                                    240  
 Glu Asn Cys Ala Lys Glu Val Ile Ala Ile Val Thr His Gly Ile Phe  
                                     245                                    250                                    255  
 Ser Gly Gly Ala Arg Glu Lys Leu Arg Asn Ser Lys Leu Ala Arg Ile  
                                     260                                    265                                    270  
 Val Ser Thr Asn Thr Val Pro Val Asp Leu Asn Leu Asp Ile Tyr His  
                                     275                                    280                                    285  
 Gln Ile Asp Ile Ser Ala Ile Leu Ala Glu Ala Ile Arg Arg Leu His  
                                     290                                    295                                    300  
 Asn Gly Glu Ser Val Ser Tyr Leu Phe Asn Asn Ala Val Met  
                                     305                                    310                                    315

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5369 base pairs

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(ix) FEATURES:

(A) NAME/KEY: 5'UTR

(B) LOCATION: 1..54

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) LOCATION: 55..1482

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) LOCATION: 1767..3299

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) LOCATION: 3588..4703

(ix) FEATURES:

(A) NAME/KEY: 3'UTR

(B) LOCATION: 4704..5369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGCTTGACC TTGGCTGGCA CTTGAGTCGG CAGACAGGTG GACTAACCCG AGCA ATG	57
Met	
1	
GAT CGT GGT TGT AAA GGT ATC TCT TAT GTG CTC AGT GCA ATG GTT TTT	105
Asp Arg Gly Cys Lys Gly Ile Ser Tyr Val Leu Ser Ala Met Val Phe	
5 10 15	
CAC ATA ATA CCG ATT ACA TTT GAA ATA TCG ATG GTA TGT GGC ATA TTG	153
His Ile Ile Pro Ile Thr Phe Glu Ile Ser Met Val Cys Gly Ile Leu	
20 25 30	

ACA TAC CAG TTT GGT GCT TCC TTC GCT GCT ATA ACA TTC TCG ACT ATG	201
Thr Tyr Gln Phe Gly Ala Ser Phe Ala Ala Ile Thr Phe Ser Thr Met	
35 40 45	
CTT CTT TAC TCC ATC TTT ACT TTC AGA ACG ACG GCG TGG CGC ACA CGG	249
Leu Leu Tyr Ser Ile Phe Thr Phe Arg Thr Thr Ala Trp Arg Thr Arg	
50 55 60 65	
TTT AGG CGT GAT GCG AAC AAG GCT GAC AAT AAG GCC GCT AGT GTG GCA	297
Phe Arg Arg Asp Ala Asn Lys Ala Asp Asn Lys Ala Ala Ser Val Ala	
70 75 80	
TTG GAT TCC CTA ATA AAT TTT GAA GCT GTA AAG TAT TTC AAT AAC GAG	345
Leu Asp Ser Leu Ile Asn Phe Glu Ala Val Lys Tyr Phe Asn Asn Glu	
85 90 95	
AAG TAC CTT GCG GAC AAG TAT CAC ACA TCC TTG ATG AAG TAC CGG GAT	393
Lys Tyr Leu Ala Asp Lys Tyr His Thr Ser Leu Met Lys Tyr Arg Asp	
100 105 110	
TCC CAG ATA AAG GTC TCG CAA TCG CTG GCG TTT TTG AAC ACC GGC CAG	441
Ser Gln Ile Lys Val Ser Gln Ser Leu Ala Phe Leu Asn Thr Gly Gln	
115 120 125	
AAC CTA ATT TTT ACC ACT GCA CTG ACT GCA ATG ATG TAT ATG GCC TGT	489
Asn Leu Ile Phe Thr Thr Ala Leu Thr Ala Met Met Tyr Met Ala Cys	
130 135 140 145	
AAT GGT GTT ATG CAG GGC TCT CTT ACA GTG GGG GAT CTT GTG TTA ATT	537
Asn Gly Val Met Gln Gly Ser Leu Thr Val Gly Asp Leu Val Leu Ile	
150 155 160	
AAT CAA CTG GTA TTC CAG CTC TCC GTG CCA CTA AAC TTC CTT GGT AGC	585
Asn Gln Leu Val Phe Gln Leu Ser Val Pro Leu Asn Phe Leu Gly Ser	
165 170 175	
GTC TAC CGT GAT CTC AAG CAG TCT CTG ATA GAT ATG GAA TCT TTA TTT	633
Val Tyr Arg Asp Leu Lys Gln Ser Leu Ile Asp Met Glu Ser Leu Phe	
180 185 190	
AAA CTG CAA AAA AAT CAG GTC ACA ATT AAG AAC TCC CCA AAT GCC CAG	681
Lys Leu Gln Lys Asn Gln Val Thr Ile Lys Asn Ser Pro Asn Ala Gln	
195 200 205	
AAC CTA CCA ATA CAC AAA CCG TTG GAT ATT CGC TTT GAA AAT GTT ACG	729
Asn Leu Pro Ile His Lys Pro Leu Asp Ile Arg Phe Glu Asn Val Thr	
210 215 220 225	

TTT GGC TAT GAC CCG GAG CGG CGT ATA TTG AAC AAT GTT TCG TTT ACC	777
Phe Gly Tyr Asp Pro Glu Arg Arg Ile Leu Asn Asn Val Ser Phe Thr	
230 235 240	
ATC CCA GCT GGA ATG AAG ACT GCC ATA GTA GGC CCA TCG GGC TCG GGG	825
Ile Pro Ala Gly Met Lys Thr Ala Ile Val Gly Pro Ser Gly Ser Gly	
245 250 255	
AAG TCC ACC ATT TTG AAG CTC GTA TTT AGA TTC TAT GAG CCC GAG CAA	873
Lys Ser Thr Ile Leu Lys Leu Val Phe Arg Phe Tyr Glu Pro Glu Gln	
260 265 270	
GGT CGT ATC CTA GTT GGC GGC ACA GAT ATC CGC GAT TTA GAC TTG CTT	921
Gly Arg Ile Leu Val Gly Gly Thr Asp Ile Arg Asp Leu Asp Leu Leu	
275 280 285	
TCT TTA CGG AAG GCT ATC GGT GTC GTG CCC CAA GAT ACT CCT CTC TTC	969
Ser Leu Arg Lys Ala Ile Gly Val Val Pro Gln Asp Thr Pro Leu Phe	
290 295 300 305	
AAT GAC ACA ATC TGG GAG AAT GTT AAA TTC GGC AAT ATC AGT TCC TCT	1017
Asn Asp Thr Ile Trp Glu Asn Val Lys Phe Gly Asn Ile Ser Ser Ser	
310 315 320	
GAC GAT GAG ATT CTC AGG GCC ATA GAA AAA GCT CAA CTC ACG AAG CTA	1065
Asp Asp Glu Ile Leu Arg Ala Ile Glu Lys Ala Gln Leu Thr Lys Leu	
325 330 335	
CTC CAG AAC CTA CCA AAG GGC GCT TCC ACC GTT GTA GGG GAG CGC GGT	1113
Leu Gln Asn Leu Pro Lys Gly Ala Ser Thr Val Val Gly Glu Arg Gly	
340 345 350	
TTG ATG ATC AGC GGA GGT GAG AAA CAA AGG CTT GCT ATT GCT CGT GTG	1161
Leu Met Ile Ser Gly Gly Glu Lys Gln Arg Leu Ala Ile Ala Arg Val	
355 360 365	
CTT TTG AAG GAC GCT CCG CTG ATG TTT TTC GAC GAG GCT ACA AGT GCT	1209
Leu Leu Lys Asp Ala Pro Leu Met Phe Phe Asp Glu Ala Thr Ser Ala	
370 375 380 385	
CTG GAT ACA CAC ACA GAG CAG GCA CTC TTG CAC ACC APT CAG CAG AAC	1257
Leu Asp Thr His Thr Glu Gln Ala Leu Leu His Thr Ile Gln Gln Asn	
390 395 400	
TTT TCT TCC AAT TCA AAG ACG AGC GTT TAC GTT GCC CAT AGA CTG CGC	1305
Phe Ser Ser Asn Ser Lys Thr Ser Val Tyr Val Ala His Arg Leu Arg	
405 410 415	



ACA ATC GCT GAT GCA GAT AAG ATC ATT GTT CTT GAA CAA GGT TCT GTC 1353  
 Thr Ile Ala Asp Ala Asp Lys Ile Ile Val Leu Glu Gln Gly Ser Val  
 420 425 430

CGC GAA GAG GGC ACA CAC AGC TCG CTG TTA GCG TCA CAA GGA TCC CTA 1401  
 Arg Glu Glu Gly Thr His Ser Ser Leu Leu Ala Ser Gln Gly Ser Leu  
 435 440 445

TAC CGG GGT CTG TGG GAT ATT CAG GAA AAC CTA ACG CTT CCG GAA CGG 1449  
 Tyr Arg Gly Leu Trp Asp Ile Gln Glu Asn Leu Thr Leu Pro Glu Arg  
 450 455 460 465

CCT GAG CAG TCA ACC GGA TCT CAG CAT GCA TAGACGTCTG ACTAGAGATT 1499  
 Pro Glu Gln Ser Thr Gly Ser Gln His Ala  
 470 475

ATATAATAAC CCTCGAGCCA AAATTATACG GCGCTAACAA GTAAAAATTT TAGTTACTTT 1559

TCTGACTTCT CTACGCTGAC TTCTCTACCC TTCTAACATA GTTAATTGAA GTAGTGGTTA 1619

ATGACGACTG CATTTTATTA TTGTCCACTT TGCATTAGAA GTACTAGTGC TTAAGCGCTC 1679

TTTAGGCCGC TTTCTTCTTC TTTGTTCAGGC CGCAAGGTAA AGGAAGCACC AACGGATTGC 1739

TACCGCTGCT ATTCCTGCTC TCTCAAG ATG TGT GGC ATA TTA GGC GTT GTG 1790  
 Met Cys Gly Ile Leu Gly Val Val  
 1 5

CTA GCC GAT CAG TCG AAG GTG GTC GCC CCT GAG TTG TTT GAT GGC TCA 1838  
 Leu Ala Asp Gln Ser Lys Val Val Ala Pro Glu Leu Phe Asp Gly Ser  
 10 15 20

CTG TTC TTA CAG CAT CGC GGT CAA GAT GCT GCC GGG ATT GCT ACG TGC 1886  
 Leu Phe Leu Gln His Arg Gly Gln Asp Ala Ala Gly Ile Ala Thr Cys  
 25 30 35 40

GGC CCC GGT GGG CGC TTG TAC CAA TGT AAG GGC AAT GGT ATG GCA CGG 1934  
 Gly Pro Gly Gly Arg Leu Tyr Gln Cys Lys Gly Asn Gly Met Ala Arg  
 45 50 55

GAC GTG TTC ACG CAA GCT CGG ATG TCA GGG TTG GTT GGC TCT ATG GGG 1982  
 Asp Val Phe Thr Gln Ala Arg Met Ser Gly Leu Val Gly Ser Met Gly  
 60 65 70

ATT GCA CAC CTG AGA TAT CCC ACT GCA GGC TCC AGT GCG AAC TCA GAA 2030  
 Ile Ala His Leu Arg Tyr Pro Thr Ala Gly Ser Ser Ala Asn Ser Glu  
 75 80 85

205720 257200T  
 10076157 024502

GCG CAG CCA TTC TAT GTG AAT AGT CCC TAC GGA ATT TGC ATG AGT CAT	2078
Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly Ile Cys Met Ser His	
90 95 100	
AAT GGT AAT CTG GTG AAC ACG ATG TCT CTA CGT AGA TAT CTT GAT GAA	2126
Asn Gly Asn Leu Val Asn Thr Met Ser Leu Arg Arg Tyr Leu Asp Glu	
105 110 115 120	
GAC GTT CAC CGT CAT ATT AAC ACG GAC AGC GAT TCT GAG CTA CTG CTT	2174
Asp Val His Arg His Ile Asn Thr Asp Ser Asp Ser Glu Leu Leu Leu	
125 130 135	
AAT ATA TTT GCC GCG GAG CTG GAA AAG TAC AAC AAA TAT CGT GTG AAC	2222
Asn Ile Phe Ala Ala Glu Leu Glu Lys Tyr Asn Lys Tyr Arg Val Asn	
140 145 150	
AAC GAT GAT ATA TTT TGT GCT CTA GAG GGT GTT TAC AAA CGT TGT CGC	2270
Asn Asp Asp Ile Phe Cys Ala Leu Glu Gly Val Tyr Lys Arg Cys Arg	
155 160 165	
GGT GGC TAT GCT TGT GTT GGC ATG TTG GCG GGA TAT GGA TTG TTT GGT	2318
Gly Gly Tyr Ala Cys Val Gly Met Leu Ala Gly Tyr Gly Leu Phe Gly	
170 175 180	
TTC CGG GAC CCC AAT GGG ATC AGG CCG CTA TTG TTT GGT GAG CGC GTC	2366
Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Leu Phe Gly Glu Arg Val	
185 190 195 200	
AAC GAT GAC GGC ACC ATG GAC TAC ATG CTA GCG TCC GAA AGT GTC GTT	2414
Asn Asp Asp Gly Thr Met Asp Tyr Met Leu Ala Ser Glu Ser Val Val	
205 210 215	
CTT AAG GCC CAC CGC TTC CAA AAC ATA CGT GAT ATT CTT CCC GGC CAA	2462
Leu Lys Ala His Arg Phe Gln Asn Ile Arg Asp Ile Leu Pro Gly Gln	
220 225 230	
GCC GTC ATT ATC CCT AAA ACG TGC GGC TCC AGT CCA CCA GAG TTC CGG	2510
Ala Val Ile Ile Pro Lys Thr Cys Gly Ser Ser Pro Pro Glu Phe Arg	
235 240 245	
CAG GTA GTG CCA ATT GAG GCC TAC AAA CCG GAC TTG TTT GAG TAC GTG	2558
Gln Val Val Pro Ile Glu Ala Tyr Lys Pro Asp Leu Phe Glu Tyr Val	
250 255 260	
TAT TTC GCT CGT GCT GAC AGC GTT CTG GAC GGT ATT TCC GTT TAC CAT	2606
Tyr Phe Ala Arg Ala Asp Ser Val Leu Asp Gly Ile Ser Val Tyr His	
265 270 275 280	

ACA	CGC	CTG	TTG	ATG	GGT	ATC	AAA	CTT	GCC	GAG	AAC	ATC	AAA	AAA	CAG	2654
Thr	Arg	Leu	Leu	Met	Gly	Ile	Lys	Leu	Ala	Glu	Asn	Ile	Lys	Lys	Gln	
				285					290						295	
ATC	GAT	CTG	GAC	GAA	ATT	GAC	GTT	GTT	GTA	TCT	GTT	CCT	GAC	ACT	GCA	2702
Ile	Asp	Leu	Asp	Glu	Ile	Asp	Val	Val	Val	Ser	Val	Pro	Asp	Thr	Ala	
				300				305					310			
CGT	ACC	TGT	GCA	TTG	GAG	TGT	GCC	AAC	CAT	TTA	AAC	AAA	CCT	TAT	CGC	2750
Arg	Thr	Cys	Ala	Leu	Glu	Cys	Ala	Asn	His	Leu	Asn	Lys	Pro	Tyr	Arg	
			315				320					325				
GAA	GGA	TTT	GTC	AAG	AAC	AGA	TAT	GTT	GGA	AGA	ACA	TTT	ATC	ATG	CCA	2798
Glu	Gly	Phe	Val	Lys	Asn	Arg	Tyr	Val	Gly	Arg	Thr	Phe	Ile	Met	Pro	
			330				335					340				
AAC	CAA	AAA	GAG	CGA	GTA	TCT	TCT	GTG	CGC	CGC	AAG	TTG	AAC	CCA	ATG	2846
Asn	Gln	Lys	Glu	Arg	Val	Ser	Ser	Val	Arg	Arg	Lys	Leu	Asn	Pro	Met	
					345		350			355					360	
AAC	TCA	GAA	TTT	AAA	GAC	AAG	CGC	GTG	CTG	ATT	GTC	GAT	GAT	TCC	ATT	2894
Asn	Ser	Glu	Phe	Lys	Asp	Lys	Arg	Val	Leu	Ile	Val	Asp	Asp	Ser	Ile	
				365				370						375		
GTG	CGA	GGT	ACC	ACT	TCC	AAA	GAG	ATT	GTT	AAC	ATG	GCG	AAG	GAA	TCC	2942
Val	Arg	Gly	Thr	Thr	Ser	Lys	Glu	Ile	Val	Asn	Met	Ala	Lys	Glu	Ser	
				380				385					390			
GGT	GCT	GCC	AAG	GTC	TAC	TTT	GCC	TCT	GCA	GCG	CCA	GCA	ATT	CGT	TTC	2990
Gly	Ala	Ala	Lys	Val	Tyr	Phe	Ala	Ser	Ala	Ala	Pro	Ala	Ile	Arg	Phe	
			395				400					405				
AAT	CAC	ATC	TAC	GGG	ATT	GAC	CTA	GCA	GAT	ACT	AAG	CAG	CTT	GTC	GCC	3038
Asn	His	Ile	Tyr	Gly	Ile	Asp	Leu	Ala	Asp	Thr	Lys	Gln	Leu	Val	Ala	
			410				415				420					
TAC	AAC	AGA	ACT	GTT	GAA	GAA	ATC	ACT	GCG	GAG	CTG	GGC	TGT	GAC	CGC	3086
Tyr	Asn	Arg	Thr	Val	Glu	Glu	Ile	Thr	Ala	Glu	Leu	Gly	Cys	Asp	Arg	
				425			430			435				440		
GTC	ATC	TAT	CAA	TCT	TTG	GAT	GAC	CTC	ATC	GAC	TGT	TGC	AAG	ACA	GAC	3134
Val	Ile	Tyr	Gln	Ser	Leu	Asp	Asp	Leu	Ile	Asp	Cys	Cys	Lys	Thr	Asp	
				445				450						455		
ATC	ATC	TCA	GAA	TTT	GAA	GTT	GGA	GTT	TTC	ACT	GGT	AAC	TAC	GTT	ACA	3182
Ile	Ile	Ser	Glu	Phe	Glu	Val	Gly	Val	Phe	Thr	Gly	Asn	Tyr	Val	Thr	
				460				465					470			

GGT GTT GAG GAT GTG TAC TTG CAG GAA TTA GAA CGT TGC CGC GCT CTT	3230
Gly Val Glu Asp Val Tyr Leu Gln Glu Leu Glu Arg Cys Arg Ala Leu	
475 480 485	
AAT AAC TCG AAT AAG GGT GAA GCG AAG GCC GAG GTT GAT ATT GGT CTC	3278
Asn Asn Ser Asn Lys Gly Glu Ala Lys Ala Glu Val Asp Ile Gly Leu	
490 495 500	
TAC AAT TCT GCC GAC TAT TAGCGGCGCC GTTGCCGGCA TCCGGCCCCA	3326
Tyr Asn Ser Ala Asp Tyr	
505 510	
TATATAGACT CATCGGGACC TAAAATAAGC CTTTACAGAT CATTATCTAC AAATATAGAT	3386
ACCATTAATA GCCTGACTTT CGACTTACTC CTAGCACACC CCGTTGTATC CCTGTGCTTG	3446
CTTTCTTAAA TGCCGTTGGT TAGGCTTTGG ACTTAGCGTC CCGCCCATTT TCTAGCATGT	3506
GCAGATCTAG CAAATTTGGC CTAAGACAAG AAGATCCATT CGGCACCCAC ATCCTGGAGC	3566
CAGCACACAG TGGACCCAGA C ATG AGC AGC GGC AAT ATA TGG AAG CAA TTG	3617
Met Ser Ser Gly Asn Ile Trp Lys Gln Leu	
1 5 10	
CTA GAG GAG AAT AGC GAA CAG CTG GAC CAG TCC ACT ACG GAG ACT TAC	3665
Leu Glu Glu Asn Ser Glu Gln Leu Asp Gln Ser Thr Thr Glu Thr Tyr	
15 20 25	
GTG GTA TGC TGC GAG AAC GAA GAT TCC CTT AAC CAG TTT TTG CAA CAA	3713
Val Val Cys Cys Glu Asn Glu Asp Ser Leu Asn Gln Phe Leu Gln Gln	
30 35 40	
TGT TGG CAG ATT GAC GAG GGC GAG AAG GTG ACC AAC CTG GAG CCG TTG	3761
Cys Trp Gln Ile Asp Glu Gly Glu Lys Val Thr Asn Leu Glu Pro Leu	
45 50 55	
GGA TTC TTT ACA AAG GTG GTT TCG CGC GAC GAA GAG AAC CTC CGG CTC	3809
Gly Phe Phe Thr Lys Val Val Ser Arg Asp Glu Glu Asn Leu Arg Leu	
60 65 70	
AAC GTA TAC TAT GCC AAG AGC CCA CTG GAT GCA CAG ACG CTG CAG TTT	3857
Asn Val Tyr Tyr Ala Lys Ser Pro Leu Asp Ala Gln Thr Leu Gln Phe	
75 80 85 90	
CTG GGC GTG TTC CTG CGC CAA ATG GAA ACC TCA CAA ATA CGT TGG ATC	3905
Leu Gly Val Phe Leu Arg Gln Met Glu Thr Ser Gln Ile Arg Trp Ile	
95 100 105	

TTC CTA CTG GAC TGG CTG CTA GAC GAT AAA CGA TTA TGG CTA CGT CAA	3953
Phe Leu Leu Asp Trp Leu Leu Asp Asp Lys Arg Leu Trp Leu Arg Gln	
110 115 120	
CTG CGG AAC TCG TGG GCC GCC TTG GAG GAA GCG CAG GTG GCA CCC TTT	4001
Leu Arg Asn Ser Trp Ala Ala Leu Glu Glu Ala Gln Val Ala Pro Phe	
125 130 135	
CCA GGT GGC GCT GTG GTG GTG GTC CTC AAC CCG AGT CAC GTG ACA CAA	4049
Pro Gly Gly Ala Val Val Val Val Leu Asn Pro Ser His Val Thr Gln	
140 145 150	
CTG GAG CGA AAC ACG ATG GTT TGG AAC TCC CGC CGT CTG GAC CTG GTA	4097
Leu Glu Arg Asn Thr Met Val Trp Asn Ser Arg Arg Leu Asp Leu Val	
155 160 165 170	
CAC CAG ACA CTG CGA GCT GCA TGC CTC AAC ACC GGC TCG GCG CTA GTT	4145
His Gln Thr Leu Arg Ala Ala Cys Leu Asn Thr Gly Ser Ala Leu Val	
175 180 185	
ACA CTT GAT CCT AAT ACT GCG CGC GAA GAC GTC ATG CAC ATA TGT GCG	4193
Thr Leu Asp Pro Asn Thr Ala Arg Glu Asp Val Met His Ile Cys Ala	
190 195 200	
CTG CTT GCG GGG CTG CCT ACA TCC CGT CCC GTC GCG ATG CTA AGC CTG	4241
Leu Leu Ala Gly Leu Pro Thr Ser Arg Pro Val Ala Met Leu Ser Leu	
205 210 215	
CAA AGT CTA TTC ATC CCC CAC GGT GCA GAT TCC ATC GGC AAG ATC TGC	4289
Gln Ser Leu Phe Ile Pro His Gly Ala Asp Ser Ile Gly Lys Ile Cys	
220 225 230	
ACC ATC GCG CCC GAG TTC CCT GTT GCT ACG GTG TTC GAC AAC GAT TTT	4337
Thr Ile Ala Pro Glu Phe Pro Val Ala Thr Val Phe Asp Asn Asp Phe	
235 240 245 250	
GTG AGC TCG ACA TTC GAG GCC GCA ATT GCT CCA GAA CTT ACT CCA GGA	4385
Val Ser Ser Thr Phe Glu Ala Ala Ile Ala Pro Glu Leu Thr Pro Gly	
255 260 265	
CCA CGT GTG CCA TCT GAC CAC CCA TGG CTA ACA GAG CCT ACC AAC CCC	4433
Pro Arg Val Pro Ser Asp His Pro Trp Leu Thr Glu Pro Thr Asn Pro	
270 275 280	
CCT TCG GAG GCA ACC GCT TGG CAT TTC GAT CTC CAA GGT CGC CTC GCT	4481
Pro Ser Glu Ala Thr Ala Trp His Phe Asp Leu Gln Gly Arg Leu Ala	
285 290 295	

ACC CTA TAC CGG CAT CTT GGT GAC TCT AAC AAG GCC ATA TCT GTT ACT 4529  
 Thr Leu Tyr Arg His Leu Gly Asp Ser Asn Lys Ala Ile Ser Val Thr  
 300 305 310

CAG CAC CGC TTC CAC AAG CCC CGC TCG GAA GAT TAT GCA TAC GAA TTC 4577  
 Gln His Arg Phe His Lys Pro Arg Ser Glu Asp Tyr Ala Tyr Glu Phe  
 315 320 325 330

GAG CTG CCG TCT AAG CAC CCT ACA ATA CGT GAC CTC ATA CGC TCT GCC 4625  
 Glu Leu Pro Ser Lys His Pro Thr Ile Arg Asp Leu Ile Arg Ser Ala  
 335 340 345

GCA GCC GAC TCA CCG AAC GAC GTC GCT GAC TCC ATC GAT GGG CTT ATG 4673  
 Ala Ala Asp Ser Pro Asn Asp Val Ala Asp Ser Ile Asp Gly Leu Met  
 350 355 360

GAT GGT ATC GTA CAA AGG AAT GTT CAT TGACGTCGAC AAAAAATTT 4720  
 Asp Gly Ile Val Gln Arg Asn Val His  
 365 370

TGTTACTGTT CTCTCGAGAA CTATTCTCAT CCAGTACTGA CATATTAGAA GGCGAAGTGA 4780

ACTAGGATTT ATATAAAGTA GCCTTCAGGC AATTGCACAG GGTCTATTGA GTCGCTGCCG 4840

TTCACGAGAG AGCCCAATAT ATCGAGGACT AATTGGTCAC TTTTGTTTTG CTATACTCAC 4900

CCTGTATTTG CTAATCATTT ATCCGCTTTG TCCAAGTGGT TGCGAAGATA TCGAGCCAGA 4960

ACATTAGAAT CTGGTTTGCC GCATCCTAGA GCTGTCTCCA AGCCAGTTGA ACCGTTGCGG 5020

GAGATTACCG CAGCCGGTTT GATCAGAGTA CTGGTGACTG CCAGCACCCA CGTTTGTGAC 5080

TTATAAATAT ACGCCCTGTG GAGCCATAGC CATTGGCATA AAGAGAAGAG CACCCCGTGC 5140

CACGATGCAG ACACTTCCGG TGTACCCAGC GTCACAGACT GCGTCGCCTA CGAAGCGTGA 5200

ACTTGCAGCG GCGCCCTCGG TGCCGCAGGA CGGCGCCCGG CTGCCTGCGC AGCTCACTTT 5260

AGTGACGCCC CCAGAACCTG ATATCCAGAA GAAGTCAGTG CGATCTCAGG TCGCGCGTTT 5320

AAGCATCTCG GAGACAGATG TAGTGAAGAG TGATATCGTG GCTAAGCTT 5369

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Asp Arg Gly Cys Lys Gly Ile Ser Tyr Val Leu Ser Ala Met Val  
 1 5 10 15  
 Phe His Ile Ile Pro Ile Thr Phe Glu Ile Ser Met Val Cys Gly Ile  
 20 25 30  
 Leu Thr Tyr Gln Phe Gly Ala Ser Phe Ala Ala Ile Thr Phe Ser Thr  
 35 40 45  
 Met Leu Leu Tyr Ser Ile Phe Thr Phe Arg Thr Thr Ala Trp Arg Thr  
 50 55 60  
 Arg Phe Arg Arg Asp Ala Asn Lys Ala Asp Asn Lys Ala Ala Ser Val  
 65 70 75 80  
 Ala Leu Asp Ser Leu Ile Asn Phe Glu Ala Val Lys Tyr Phe Asn Asn  
 85 90 95  
 Glu Lys Tyr Leu Ala Asp Lys Tyr His Thr Ser Leu Met Lys Tyr Arg  
 100 105 110  
 Asp Ser Gln Ile Lys Val Ser Gln Ser Leu Ala Phe Leu Asn Thr Gly  
 115 120 125  
 Gln Asn Leu Ile Phe Thr Thr Ala Leu Thr Ala Met Met Tyr Met Ala  
 130 135 140  
 Cys Asn Gly Val Met Gln Gly Ser Leu Thr Val Gly Asp Leu Val Leu  
 145 150 155 160  
 Ile Asn Gln Leu Val Phe Gln Leu Ser Val Pro Leu Asn Phe Leu Gly  
 165 170 175  
 Ser Val Tyr Arg Asp Leu Lys Gln Ser Leu Ile Asp Met Glu Ser Leu  
 180 185 190  
 Phe Lys Leu Gln Lys Asn Gln Val Thr Ile Lys Asn Ser Pro Asn Ala  
 195 200 205  
 Gln Asn Leu Pro Ile His Lys Pro Leu Asp Ile Arg Phe Glu Asn Val  
 210 215 220  
 Thr Phe Gly Tyr Asp Pro Glu Arg Arg Ile Leu Asn Asn Val Ser Phe  
 225 230 235 240

10076457.021502

Thr Ile Pro Ala Gly Met Lys Thr Ala Ile Val Gly Pro Ser Gly Ser  
 245 250 255  
 Gly Lys Ser Thr Ile Leu Lys Leu Val Phe Arg Phe Tyr Glu Pro Glu  
 260 265 270  
 Gln Gly Arg Ile Leu Val Gly Gly Thr Asp Ile Arg Asp Leu Asp Leu  
 275 280 285  
 Leu Ser Leu Arg Lys Ala Ile Gly Val Val Pro Gln Asp Thr Pro Leu  
 290 295 300  
 Phe Asn Asp Thr Ile Trp Glu Asn Val Lys Phe Gly Asn Ile Ser Ser  
 305 310 315 320  
 Ser Asp Asp Glu Ile Leu Arg Ala Ile Glu Lys Ala Gln Leu Thr Lys  
 325 330 335  
 Leu Leu Gln Asn Leu Pro Lys Gly Ala Ser Thr Val Val Gly Glu Arg  
 340 345 350  
 Gly Leu Met Ile Ser Gly Gly Glu Lys Gln Arg Leu Ala Ile Ala Arg  
 355 360 365  
 Val Leu Leu Lys Asp Ala Pro Leu Met Phe Phe Asp Glu Ala Thr Ser  
 370 375 380  
 Ala Leu Asp Thr His Thr Glu Gln Ala Leu Leu His Thr Ile Gln Gln  
 385 390 395 400  
 Asn Phe Ser Ser Asn Ser Lys Thr Ser Val Tyr Val Ala His Arg Leu  
 405 410 415  
 Arg Thr Ile Ala Asp Ala Asp Lys Ile Ile Val Leu Glu Gln Gly Ser  
 420 425 430  
 Val Arg Glu Glu Gly Thr His Ser Ser Leu Leu Ala Ser Gln Gly Ser  
 435 440 445  
 Leu Tyr Arg Gly Leu Trp Asp Ile Gln Glu Asn Leu Thr Leu Pro Glu  
 450 455 460  
 Arg Pro Glu Gln Ser Thr Gly Ser Gln His Ala  
 465 470 475

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 Amino acids

10076157-021502



(B) TYPE: Amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met	Cys	Gly	Ile	Leu	Gly	Val	Val	Leu	Ala	Asp	Gln	Ser	Lys	Val	Val	1	5	10	15
Ala	Pro	Glu	Leu	Phe	Asp	Gly	Ser	Leu	Phe	Leu	Gln	His	Arg	Gly	Gln	20	25	30	
Asp	Ala	Ala	Gly	Ile	Ala	Thr	Cys	Gly	Pro	Gly	Gly	Arg	Leu	Tyr	Gln	35	40	45	
Cys	Lys	Gly	Asn	Gly	Met	Ala	Arg	Asp	Val	Phe	Thr	Gln	Ala	Arg	Met	50	55	60	
Ser	Gly	Leu	Val	Gly	Ser	Met	Gly	Ile	Ala	His	Leu	Arg	Tyr	Pro	Thr	65	70	75	80
Ala	Gly	Ser	Ser	Ala	Asn	Ser	Glu	Ala	Gln	Pro	Phe	Tyr	Val	Asn	Ser	85	90	95	
Pro	Tyr	Gly	Ile	Cys	Met	Ser	His	Asn	Gly	Asn	Leu	Val	Asn	Thr	Met	100	105	110	
Ser	Leu	Arg	Arg	Tyr	Leu	Asp	Glu	Asp	Val	His	Arg	His	Ile	Asn	Thr	115	120	125	
Asp	Ser	Asp	Ser	Glu	Leu	Leu	Leu	Asn	Ile	Phe	Ala	Ala	Glu	Leu	Glu	130	135	140	
Lys	Tyr	Asn	Lys	Tyr	Arg	Val	Asn	Asn	Asp	Asp	Ile	Phe	Cys	Ala	Leu	145	150	155	160
Glu	Gly	Val	Tyr	Lys	Arg	Cys	Arg	Gly	Gly	Tyr	Ala	Cys	Val	Gly	Met	165	170	175	
Leu	Ala	Gly	Tyr	Gly	Leu	Phe	Gly	Phe	Arg	Asp	Pro	Asn	Gly	Ile	Arg	180	185	190	
Pro	Leu	Leu	Phe	Gly	Glu	Arg	Val	Asn	Asp	Asp	Gly	Thr	Met	Asp	Tyr	195	200	205	
Met	Leu	Ala	Ser	Glu	Ser	Val	Val	Leu	Lys	Ala	His	Arg	Phe	Gln	Asn	210	215	220	

1007647.021502

Ile Arg Asp Ile Leu Pro Gly Gln Ala Val Ile Ile Pro Lys Thr Cys  
 225 230 235 240  
 Gly Ser Ser Pro Pro Glu Phe Arg Gln Val Val Pro Ile Glu Ala Tyr  
 245 250 255  
 Lys Pro Asp Leu Phe Glu Tyr Val Tyr Phe Ala Arg Ala Asp Ser Val  
 260 265 270  
 Leu Asp Gly Ile Ser Val Tyr His Thr Arg Leu Leu Met Gly Ile Lys  
 275 280 285  
 Leu Ala Glu Asn Ile Lys Lys Gln Ile Asp Leu Asp Glu Ile Asp Val  
 290 295 300  
 Val Val Ser Val Pro Asp Thr Ala Arg Thr Cys Ala Leu Glu Cys Ala  
 305 310 315 320  
 Asn His Leu Asn Lys Pro Tyr Arg Glu Gly Phe Val Lys Asn Arg Tyr  
 325 330 335  
 Val Gly Arg Thr Phe Ile Met Pro Asn Gln Lys Glu Arg Val Ser Ser  
 340 345 350  
 Val Arg Arg Lys Leu Asn Pro Met Asn Ser Glu Phe Lys Asp Lys Arg  
 355 360 365  
 Val Leu Ile Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Lys Glu  
 370 375 380  
 Ile Val Asn Met Ala Lys Glu Ser Gly Ala Ala Lys Val Tyr Phe Ala  
 385 390 395 400  
 Ser Ala Ala Pro Ala Ile Arg Phe Asn His Ile Tyr Gly Ile Asp Leu  
 405 410 415  
 Ala Asp Thr Lys Gln Leu Val Ala Tyr Asn Arg Thr Val Glu Glu Ile  
 420 425 430  
 Thr Ala Glu Leu Gly Cys Asp Arg Val Ile Tyr Gln Ser Leu Asp Asp  
 435 440 445  
 Leu Ile Asp Cys Cys Lys Thr Asp Ile Ile Ser Glu Phe Glu Val Gly  
 450 455 460  
 Val Phe Thr Gly Asn Tyr Val Thr Gly Val Glu Asp Val Tyr Leu Gln  
 465 470 475 480  
 Glu Leu Glu Arg Cys Arg Ala Leu Asn Asn Ser Asn Lys Gly Glu Ala  
 485 490 495

1006157-024502

Lys Ala Glu Val Asp Ile Gly Leu Tyr Asn Ser Ala Asp Tyr  
                   500                                  505                                  510

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Ser	Ser	Gly	Asn	Ile	Trp	Lys	Gln	Leu	Leu	Glu	Glu	Asn	Ser	Glu	1	5	10	15
Gln	Leu	Asp	Gln	Ser	Thr	Thr	Glu	Thr	Tyr	Val	Val	Cys	Cys	Glu	Asn	20	25	30	
Glu	Asp	Ser	Leu	Asn	Gln	Phe	Leu	Gln	Gln	Cys	Trp	Gln	Ile	Asp	Glu	35	40	45	
Gly	Glu	Lys	Val	Thr	Asn	Leu	Glu	Pro	Leu	Gly	Phe	Phe	Thr	Lys	Val	50	55	60	
Val	Ser	Arg	Asp	Glu	Glu	Asn	Leu	Arg	Leu	Asn	Val	Tyr	Tyr	Ala	Lys	65	70	75	80
Ser	Pro	Leu	Asp	Ala	Gln	Thr	Leu	Gln	Phe	Leu	Gly	Val	Phe	Leu	Arg	85	90	95	
Gln	Met	Glu	Thr	Ser	Gln	Ile	Arg	Trp	Ile	Phe	Leu	Leu	Asp	Trp	Leu	100	105	110	
Leu	Asp	Asp	Lys	Arg	Leu	Trp	Leu	Arg	Gln	Leu	Arg	Asn	Ser	Trp	Ala	115	120	125	
Ala	Leu	Glu	Glu	Ala	Gln	Val	Ala	Pro	Phe	Pro	Gly	Gly	Ala	Val	Val	130	135	140	
Val	Val	Leu	Asn	Pro	Ser	His	Val	Thr	Gln	Leu	Glu	Arg	Asn	Thr	Met	145	150	155	160
Val	Trp	Asn	Ser	Arg	Arg	Leu	Asp	Leu	Val	His	Gln	Thr	Leu	Arg	Ala	165	170	175	

Ala Cys Leu Asn Thr Gly Ser Ala Leu Val Thr Leu Asp Pro Asn Thr  
 180 185 190  
 Ala Arg Glu Asp Val Met His Ile Cys Ala Leu Leu Ala Gly Leu Pro  
 195 200 205  
 Thr Ser Arg Pro Val Ala Met Leu Ser Leu Gln Ser Leu Phe Ile Pro  
 210 215 220  
 His Gly Ala Asp Ser Ile Gly Lys Ile Cys Thr Ile Ala Pro Glu Phe  
 225 230 235 240  
 Pro Val Ala Thr Val Phe Asp Asn Asp Phe Val Ser Ser Thr Phe Glu  
 245 250 255  
 Ala Ala Ile Ala Pro Glu Leu Thr Pro Gly Pro Arg Val Pro Ser Asp  
 260 265 270  
 His Pro Trp Leu Thr Glu Pro Thr Asn Pro Pro Ser Glu Ala Thr Ala  
 275 280 285  
 Trp His Phe Asp Leu Gln Gly Arg Leu Ala Thr Leu Tyr Arg His Leu  
 290 295 300  
 Gly Asp Ser Asn Lys Ala Ile Ser Val Thr Gln His Arg Phe His Lys  
 305 310 315 320  
 Pro Arg Ser Glu Asp Tyr Ala Tyr Glu Phe Glu Leu Pro Ser Lys His  
 325 330 335  
 Pro Thr Ile Arg Asp Leu Ile Arg Ser Ala Ala Ala Asp Ser Pro Asn  
 340 345 350  
 Asp Val Ala Asp Ser Ile Asp Gly Leu Met Asp Gly Ile Val Gln Arg  
 355 360 365  
 Asn Val His  
 370

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3616 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(ix) FEATURES:

(A) NAME/KEY: 5'UTR

(B) LOCATION: 1..863

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) LOCATION: 864..1316

(ix) FEATURES:

(A) NAME/KEY: intron

(B) LOCATION: 1317..1477

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) LOCATION 1478..2592

(ix) FEATURES:

(A) NAME/KEY: 3'UTR

(B) LOCATION: 2593..3616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGGCCCCGGTG CCAGCTCGCC AGGTGCGGAC TCGCGCTCGG GCTGTGGGCG CTCTACCTGC	60
TGCTGCTCGG CAGCTGCCTG ACGCGCGCGT ACGAGCTGTC GGATCTCGAA AACCTGGAAT	120
CCGATTACTA CAGCTACGTG CTGGATGTGA ACTTCGCGCT GCTGAGCGCC ATGAGCGCGA	180
CCGGCCTCGC GATGGGCGCC GTGAGCGGCT CCCTCGGGAG CGCGCCGGTG CTCGCGCAGT	240
GGCCGGCAGC GATCTGGGCC GTGCGCTTCC TCGCGCCCGC GGGCTATGTC GCGATAGTCC	300
TAATCCTGCC GTTCCTGTCC GTCGTCGCAT TCCTGCAGCC GCTCTGCGAG CGCGCGCTGG	360
CGCTGTTCCC GTTTGTGCGC GCGTGGGGCA TGGACGGCGT GTTCAACTTC CTGCTGCTCT	420
CCGCCGTGCT CTGGACTGTA TTCCTGGCCG TTCGCCTGCT CCGCGCCGTC TACAGACTGC	480
TGCGCTGGCT GGTTCGGTCTT TTGGTCCGCC TGGCACGCCT GCTGCTGCGA GGCGCCCGTC	540
GGACGCCTGC GGC GGCCCCC GAGGAGCCCG TCTAGCGTGC GCGCGTTCTA GGCCCCTGAC	600
AGCTCCTACC TGGTGCTGGC CGCCGGTAGG GCTCGCATCG TGCGGCGCAG GCCCATTGCT	660

TTTTGGCCCC CGCTGGATCA TCGTTTCTTT TACGTGAAAA GTTGCAGCG ATGAGCTGCA	720
GTATAAATAG GTTTTCTAGA TGCGCCAAAT CCCAGCTGGG TTTACCGGCG TCTGTTCGGG	780
ATAGTTACTT GATGGATGGG TCAACTTGAG AGCTTGGGTT TAGTGTTGAC TCCTTCTCTT	840
CATAGCACGC CGAACAAAGC GCA ATG ACT TAC AGA GAC GCA GCC ACG GCA	890
Met Thr Tyr Arg Asp Ala Ala Thr Ala	
1 5	
CTG GAG CAC CTG GCG ACG TAC GCC GAG AAG GAC GGG CTG TCC GTG GAG	938
Leu Glu His Leu Ala Thr Tyr Ala Glu Lys Asp Gly Leu Ser Val Glu	
10 15 20 25	
CAG TTG ATG GAC TCC AAG ACG CGG GGC GGG TTG ACG TAC AAC GAC TTC	986
Gln Leu Met Asp Ser Lys Thr Arg Gly Gly Leu Thr Tyr Asn Asp Phe	
30 35 40	
CTG GTC TTG CCG GGC AAG ATC GAC TTC CCA TCG TCG GAG GTG GTG CTG	1034
Leu Val Leu Pro Gly Lys Ile Asp Phe Pro Ser Ser Glu Val Val Leu	
45 50 55	
TCG TCG CGC CTG ACC AAG AAG ATC ACC TTG AAC GCG CCG TTT GTG TCG	1082
Ser Ser Arg Leu Thr Lys Lys Ile Thr Leu Asn Ala Pro Phe Val Ser	
60 65 70	
TCG CCG ATG GAC ACG GTG ACG GAG GCC GAC ATG GCG ATC CAC ATG GCG	1130
Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile His Met Ala	
75 80 85	
CTC CTG GGC GGC ATC GGG ATC ATC CAC CAC AAC TGC ACT GCG GAG GAG	1178
Leu Leu Gly Gly Ile Gly Ile Ile His His Asn Cys Thr Ala Glu Glu	
90 95 100 105	
CAG GCG GAG ATG GTG CGC CGG GTC AAG AAG TAC GAA AAC GGG TTC ATC	1226
Gln Ala Glu Met Val Arg Arg Val Lys Lys Tyr Glu Asn Gly Phe Ile	
110 115 120	
AAC GCC CCC GTG GTC GTG GGG CCG GAC GCG ACG GTG GCG GAC GTG CGC	1274
Asn Ala Pro Val Val Val Gly Pro Asp Ala Thr Val Ala Asp Val Arg	
125 130 135	
CGG ATG AAG AAC GAG TTT GGG TTT GCA GGA TTT CCT GTG ACA	1316
Arg Met Lys Asn Glu Phe Gly Phe Ala Gly Phe Pro Val Thr	
140 145 150	
GGTATGTTAG AGTGGCACGC GGGGCTGCAC GCTGGGATGA TGATCATAAA TCAATAACTT	1376
TCGTTCTACT GACTGCGATC AAACGATCGT GTAGACACCT TTTACTCTGA CCGCAGACGT	1436

20250720 10:07:02

GCAGCGCCTT TTTGGCAGGA ACATGTACTA ACACATCAGC A GAT GAT GGC AAG	1489
Asp Asp Gly Lys	
1	
CCG ACC GGG AAG CTG CAG GGG ATC ATC ACG TCC CGT GAC ATC CAG TTT	1537
Pro Thr Gly Lys Leu Gln Gly Ile Ile Thr Ser Arg Asp Ile Gln Phe	
5 10 15 20	
GTC GAG GAC GAG ACC CTG CTT GTG TCT GAG ATC ATG ACC AAG GAC GTC	1585
Val Glu Asp Glu Thr Leu Leu Val Ser Glu Ile Met Thr Lys Asp Val	
25 30 35	
ATC ACT GGG AAG CAG GGC ATC AAC CTC GAG GAG GCG AAC CAG ATC CTG	1633
Ile Thr Gly Lys Gln Gly Ile Asn Leu Glu Glu Ala Asn Gln Ile Leu	
40 45 50	
AAG AAC ACC AAG AAG GGC AAG CTG CCA ATT GTG GAC GAG GCG GGC TGC	1681
Lys Asn Thr Lys Lys Gly Lys Leu Pro Ile Val Asp Glu Ala Gly Cys	
55 60 65	
CTG GTG TCC ATG CTT TCG AGA ACT GAC TTG ATG AAG AAC CAG TCC TAC	1729
Leu Val Ser Met Leu Ser Arg Thr Asp Leu Met Lys Asn Gln Ser Tyr	
70 75 80	
CCA TTG GCC TCC AAG TCT GCC GAC ACC AAG CAG CTG CTC TGT GGT GCT	1777
Pro Leu Ala Ser Lys Ser Ala Asp Thr Lys Gln Leu Leu Cys Gly Ala	
85 90 95 100	
GCG ATC GGC ACC ATC GAC GCG GAC AGG CAG AGA CTG GCG ATG CTG GTC	1825
Ala Ile Gly Thr Ile Asp Ala Asp Arg Gln Arg Leu Ala Met Leu Val	
105 110 115	
GAG GCC GGT CTG GAC GTT GTT GTG CTA GAC TCC TCG CAG GGT AAC TCG	1873
Glu Ala Gly Leu Asp Val Val Val Leu Asp Ser Ser Gln Gly Asn Ser	
120 125 130	
GTC TTC CAG ATC AAC ATG ATC AAG TGG ATC AAG GAG ACC TTC CCA GAC	1921
Val Phe Gln Ile Asn Met Ile Lys Trp Ile Lys Glu Thr Phe Pro Asp	
135 140 145	
CTG CAG GTC ATT GCT GGC AAC GTG GTC ACC AGA GAG CAG GCT GCC AGC	1969
Leu Gln Val Ile Ala Gly Asn Val Val Thr Arg Glu Gln Ala Ala Ser	
150 155 160	
TTG ATC CAC GCC GGC GCA GAC GGG TTG CGT ATC GGT ATG GGC TCT GGC	2017
Leu Ile His Ala Gly Ala Asp Gly Leu Arg Ile Gly Met Gly Ser Gly	
165 170 175 180	

2025-05-10 10:00:00

TCC	ATC	TGT	ATC	ACT	CAG	GAG	GTG	ATG	GCC	TGT	GGT	AGA	CCA	CAG	GGT	2065
Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	Met	Ala	Cys	Gly	Arg	Pro	Gln	Gly	
				185					190					195		
ACC	GCT	GTC	TAC	AAC	GTC	ACG	CAG	TTC	GCC	AAC	CAG	TTT	GGT	GTG	CCA	2113
Thr	Ala	Val	Tyr	Asn	Val	Thr	Gln	Phe	Ala	Asn	Gln	Phe	Gly	Val	Pro	
			200					205					210			
TGT	ATT	GCT	GAC	GGT	GGT	GTC	CAG	AAC	ATC	GGG	CAC	ATT	ACC	AAA	GCT	2161
Cys	Ile	Ala	Asp	Gly	Gly	Val	Gln	Asn	Ile	Gly	His	Ile	Thr	Lys	Ala	
		215					220					225				
ATC	GCT	CTT	GGC	GCG	TCC	ACC	GTC	ATG	ATG	GGC	GGT	ATG	CTG	GCA	GGC	2209
Ile	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	Gly	Gly	Met	Leu	Ala	Gly	
		230					235					240				
ACT	ACA	GAG	TCT	CCA	GGC	GAG	TAC	TTC	TTC	AGG	GAC	GGG	AAG	AGA	CTG	2257
Thr	Thr	Glu	Ser	Pro	Gly	Glu	Tyr	Phe	Phe	Arg	Asp	Gly	Lys	Arg	Leu	
245					250					255					260	
AAG	ACC	TAC	AGA	GGT	ATG	GGC	TCC	ATC	GAC	GCC	ATG	CAA	AAG	ACT	GAT	2305
Lys	Thr	Tyr	Arg	Gly	Met	Gly	Ser	Ile	Asp	Ala	Met	Gln	Lys	Thr	Asp	
				265					270					275		
GTC	AAG	GGT	AAC	GCC	GCT	ACC	TCC	CGT	TAC	TTC	TCT	GAG	TCT	GAC	AAG	2353
Val	Lys	Gly	Asn	Ala	Ala	Thr	Ser	Arg	Tyr	Phe	Ser	Glu	Ser	Asp	Lys	
			280					285					290			
GTT	CTG	GTC	GCT	CAG	GGT	GTT	ACT	GGT	TCT	GTG	ATC	GAC	AAG	GGC	TCC	2401
Val	Leu	Val	Ala	Gln	Gly	Val	Thr	Gly	Ser	Val	Ile	Asp	Lys	Gly	Ser	
		295					300					305				
ATC	AAG	AAG	TAC	ATT	CCA	TAT	CTG	TAC	AAT	GGT	CTA	CAG	CAC	TCG	TGC	2449
Ile	Lys	Lys	Tyr	Ile	Pro	Tyr	Leu	Tyr	Asn	Gly	Leu	Gln	His	Ser	Cys	
		310					315				320					
CAG	GAT	ATC	GGT	GTG	CGC	TCT	CTA	GTG	GAG	TTC	AGA	GAG	AAG	GTG	GAC	2497
Gln	Asp	Ile	Gly	Val	Arg	Ser	Leu	Val	Glu	Phe	Arg	Glu	Lys	Val	Asp	
325					330				335					340		
TCT	GGC	TCG	GTC	AGA	TTT	GAG	TTC	AGA	ACT	CCA	TCT	GCC	CAG	TTG	GAG	2545
Ser	Gly	Ser	Val	Arg	Phe	Glu	Phe	Arg	Thr	Pro	Ser	Ala	Gln	Leu	Glu	
				345					350					355		
GGT	GGT	GTG	CAC	AAC	TTG	CAC	TCC	TAC	GAG	AAG	CGC	CTA	TTT	GACTGAGTGC	2597	
Gly	Gly	Val	His	Asn	Leu	His	Ser	Tyr	Glu	Lys	Arg	Leu	Phe	Asp		
			360					365					370			
CACTAGGCC	CACTATAGA	AGTGGATCCG	GGCGCGATGG	CACCCATACT	TTTATATTAT	2657										



GTTGATTGAT GTACGTAAAC GATAGATATA ATAACAGACG CGGCATCTCA TTTGTATGCA 2717  
 ATATATCTGG AACATGGTTA TGCCTACTCA ACTGTATGTA CTACTTTATA TACACAGCTC 2777  
 TGGGACACTT GGTGAGATAT ATGTTTCATT ATGTATGCCT CGCTATCGAA AGGTCTGGCA 2837  
 TTATGGGCTA CTGGGTCTAA GAGTCATGGC TTATGAGTAT TTATTTATTT ATTTCTCTTC 2897  
 CTTTTCATTA AACTCCTCGA GCTTCTTTCT GTAATACTGC TCTCTAGACT TCTCCACATC 2957  
 TGCTAATGAT GGTGGAAGTC GTTCGTTTTTC CAAATCCGCT CTACGAGCGC GCTCGAAGTT 3017  
 AGACAGCGCC TCGTTCAGAC CTTCAGACCC GCGTGACAGC GCTCCACGAG GCAGCACGCC 3077  
 AGAATTCATT GTTTTTAGGT ACTGCACCTT ATCGCTCTCT TCTCTCAACA CGCTATACAT 3137  
 TCGGGAAACC TTGGCAATCG CCAATATTTT ACTGCGTAGT GCACGCCGTT TTGCATCATC 3197  
 GTCCAGAATA GACCGTTTTT TCTTCGATTT CTTGGAGCCA GGTATAACAG TTACAACCTG 3257  
 CTCAGTGTTT TTGGACTTCA ATGTAGCACC TAAGTCCTCC CTTATAACAA AAGTCTCTTC 3317  
 CTCCAATTCT TCTTCAGTAC AAATGTTTAA TATCGAAACC AACATTTTCTC TCACTTTCTC 3377  
 GCCAACAAAT GGCAAAGACC AGGTGAATAC GTCCATGAAA TTCGGTAACC AATACGGATG 3437  
 CTGTGACATG TTAAATTGTC TAATGTTTAT AACGTTATCC GAGTATTTTA GGACCGCGGC 3497  
 CTTGTTCTTG TAAGTGTTCA AGTAGTTGGG TGCCTGAAC AACGTAAGTA AACTAGGAAA 3557  
 GCCCAGATTC TTGGTATTCT TGTACATTCT GTAGCCCTGA TCTTGGGCTT CGTGGGCCC 3616

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Thr Tyr Arg Asp Ala Ala Thr Ala Leu Glu His Leu Ala Thr Tyr  
 1 5 10 15  
 Ala Glu Lys Asp Gly Leu Ser Val Glu Gln Leu Met Asp Ser Lys Thr  
 20 25 30

Arg Gly Gly Leu Thr Tyr Asn Asp Phe Leu Val Leu Pro Gly Lys Ile  
           35                          40                          45

Asp Phe Pro Ser Ser Glu Val Val Leu Ser Ser Arg Leu Thr Lys Lys  
           50                          55                          60

Ile Thr Leu Asn Ala Pro Phe Val Ser Ser Pro Met Asp Thr Val Thr  
       65                          70                          75                          80

Glu Ala Asp Met Ala Ile His Met Ala Leu Leu Gly Gly Ile Gly Ile  
                           85                          90                          95

Ile His His Asn Cys Thr Ala Glu Glu Gln Ala Glu Met Val Arg Arg  
                   100                          105                          110

Val Lys Lys Tyr Glu Asn Gly Phe Ile Asn Ala Pro Val Val Val Gly  
           115                          120                          125

Pro Asp Ala Thr Val Ala Asp Val Arg Arg Met Lys Asn Glu Phe Gly  
       130                          135                          140

Phe Ala Gly Phe Pro Val Thr  
       145                          150

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Asp Asp Gly Lys Pro Thr Gly Lys Leu Gln Gly Ile Ile Thr Ser Arg  
       1                          5                          10                          15

Asp Ile Gln Phe Val Glu Asp Glu Thr Leu Leu Val Ser Glu Ile Met  
           20                          25                          30

Thr Lys Asp Val Ile Thr Gly Lys Gln Gly Ile Asn Leu Glu Glu Ala  
           35                          40                          45

Asn Gln Ile Leu Lys Asn Thr Lys Lys Gly Lys Leu Pro Ile Val Asp  
       50                          55                          60

Glu Ala Gly Cys Leu Val Ser Met Leu Ser Arg Thr Asp Leu Met Lys  
 65 70 75 80  
 Asn Gln Ser Tyr Pro Leu Ala Ser Lys Ser Ala Asp Thr Lys Gln Leu  
 85 90 95  
 Leu Cys Gly Ala Ala Ile Gly Thr Ile Asp Ala Asp Arg Gln Arg Leu  
 100 105 110  
 Ala Met Leu Val Glu Ala Gly Leu Asp Val Val Val Leu Asp Ser Ser  
 115 120 125  
 Gln Gly Asn Ser Val Phe Gln Ile Asn Met Ile Lys Trp Ile Lys Glu  
 130 135 140  
 Thr Phe Pro Asp Leu Gln Val Ile Ala Gly Asn Val Val Thr Arg Glu  
 145 150 155 160  
 Gln Ala Ala Ser Leu Ile His Ala Gly Ala Asp Gly Leu Arg Ile Gly  
 165 170 175  
 Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Met Ala Cys Gly  
 180 185 190  
 Arg Pro Gln Gly Thr Ala Val Tyr Asn Val Thr Gln Phe Ala Asn Gln  
 195 200 205  
 Phe Gly Val Pro Cys Ile Ala Asp Gly Gly Val Gln Asn Ile Gly His  
 210 215 220  
 Ile Thr Lys Ala Ile Ala Leu Gly Ala Ser Thr Val Met Met Gly Gly  
 225 230 235 240  
 Met Leu Ala Gly Thr Thr Glu Ser Pro Gly Glu Tyr Phe Phe Arg Asp  
 245 250 255  
 Gly Lys Arg Leu Lys Thr Tyr Arg Gly Met Gly Ser Ile Asp Ala Met  
 260 265 270  
 Gln Lys Thr Asp Val Lys Gly Asn Ala Ala Thr Ser Arg Tyr Phe Ser  
 275 280 285  
 Glu Ser Asp Lys Val Leu Val Ala Gln Gly Val Thr Gly Ser Val Ile  
 290 295 300  
 Asp Lys Gly Ser Ile Lys Lys Tyr Ile Pro Tyr Leu Tyr Asn Gly Leu  
 305 310 315 320  
 Gln His Ser Cys Gln Asp Ile Gly Val Arg Ser Leu Val Glu Phe Arg  
 325 330 335

Glu Lys Val Asp Ser Gly Ser Val Arg Phe Glu Phe Arg Thr Pro Ser  
 340 345 350

Ala Gln Leu Glu Gly Gly Val His Asn Leu His Ser Tyr Glu Lys Arg  
 355 360 365

Leu Phe Asp  
 370

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2697 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

- (ix) FEATURES:  
 (A) NAME/KEY: 5'UTR  
 (B) LOCATION: 1..455

- (ix) FEATURES:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 456..2033

- (ix) FEATURES:  
 (A) NAME/KEY: 3'UTR  
 (B) LOCATION: 2034..2697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ATCGATTTCA GGAGATTTTT GGTAGCATT A TTGAGGTCAT TAGAGGCGTT CTGTGACTTT	60
CGACGATTTG CACGCGCAGA AGAGGGCGTT CAACCAGCCT TTCGGATATT CCGGTTTCGAG	120
TTATACCAGC AGGGATCAGC GCAGGCACTA GAGTGGCGGG TGCTAATAAG AGGAGCAGGT	180
CCTGGAACTG AAGTTGCAAG AGATAAGCAT TGC GCGGAGA AGGAGGCGGT TAGAGGGTGC	240
AAGCGAGCAG GATGGGGTCT TCGATGAACT TCCCGTCTGG GTATGTGAAC AAGCACACGC	300

10076157.021502

TGCAGGCACA CCGGTAGGGC GAGTGCAGGG TGAAAAATAT ATATGCGCTC GAGAAGCGCT	360
GGGGATGAGT TCGTCTGCAA CGGCAGGCGG ATCTTCATCT GACAAAACCA GCTGCCTACA	420
TCAGTGCGAA GCTGTTTCAGT GATAGAATAG GAGTA ATG GCT GCT GTT GAA CAA	473
Met Ala Ala Val Glu Gln	
1 5	
GTT TCT AGC GTG TTT GAC ACC ATT TTG GTG CTG GAC TTC GGG TCC CAG	521
Val Ser Ser Val Phe Asp Thr Ile Leu Val Leu Asp Phe Gly Ser Gln	
10 15 20	
TAC TCG CAT CTG ATC ACG CGG CGG CTG CGT GAG TTT AAT GTG TAC GCG	569
Tyr Ser His Leu Ile Thr Arg Arg Leu Arg Glu Phe Asn Val Tyr Ala	
25 30 35	
GAG ATG CTT CCG TGT ACG CAG AAG ATC AGC GAG CTG GGC TGG AAG CCA	617
Glu Met Leu Pro Cys Thr Gln Lys Ile Ser Glu Leu Gly Trp Lys Pro	
40 45 50	
AAG GGT GTG ATT TTG TCA GGC GGG CCG TAC TCC GTG TAC GCG GCA GAT	665
Lys Gly Val Ile Leu Ser Gly Gly Pro Tyr Ser Val Tyr Ala Ala Asp	
55 60 65 70	
GCT CCG CAC GTG GAC CGG GCG GTG TTC GAG TTG GGC GTT CCA ATT CTG	713
Ala Pro His Val Asp Arg Ala Val Phe Glu Leu Gly Val Pro Ile Leu	
75 80 85	
GGC ATC TGC TAC GGG CTA CAG GAG CTT GCG TGG ATA GCC GGC GCA GAG	761
Gly Ile Cys Tyr Gly Leu Gln Glu Leu Ala Trp Ile Ala Gly Ala Glu	
90 95 100	
GTG GGG CGC GGC GAG AAG CGC GAG TAC GGG CGC GCG ACG CTG CAC GTG	809
Val Gly Arg Gly Glu Lys Arg Glu Tyr Gly Arg Ala Thr Leu His Val	
105 110 115	
GAG GAC AGC GCG TGC CCG CTG TTC AAC AAC GTG GAC AGC AGC ACG GTG	857
Glu Asp Ser Ala Cys Pro Leu Phe Asn Asn Val Asp Ser Ser Thr Val	
120 125 130	
TGG ATG TCG CAC GGT GAC AAG CTG CAC GCA CTA CCT GCG GAT TTC CAC	905
Trp Met Ser His Gly Asp Lys Leu His Ala Leu Pro Ala Asp Phe His	
135 140 145 150	
GTC ACT GCG ACG ACG GAG AAC TCT CCT TTC TGC GGG ATT GCA CAC GAC	953
Val Thr Ala Thr Thr Glu Asn Ser Pro Phe Cys Gly Ile Ala His Asp	
155 160 165	

TCG AAG CCA ATC TTC GGG ATC CAG TTC CAC CCT GAG GTG ACG CAC TCC	1001
Ser Lys Pro Ile Phe Gly Ile Gln Phe His Pro Glu Val Thr His Ser	
170 175 180	
TCG CAG GGG AAG ACG TTG CTG AAG AAC TTT GCG GTG GAG ATC TGC CAG	1049
Ser Gln Gly Lys Thr Leu Leu Lys Asn Phe Ala Val Glu Ile Cys Gln	
185 190 195	
GCC GCG CAG ACC TGG ACG ATG GAA AAC TTC ATT GAC ACC GAG ATC CAG	1097
Ala Ala Gln Thr Trp Thr Met Glu Asn Phe Ile Asp Thr Glu Ile Gln	
200 205 210	
CGG ATC CGG ACC CTT GTG GGC CCC ACC GCG GAA GTC ATC GGT GCT GTG	1145
Arg Ile Arg Thr Leu Val Gly Pro Thr Ala Glu Val Ile Gly Ala Val	
215 220 225 230	
TCC GGC GGT GTC GAC TCG ACC GTC GCT GCG AAG CTG ATG ACC GAG GCC	1193
Ser Gly Gly Val Asp Ser Thr Val Ala Ala Lys Leu Met Thr Glu Ala	
235 240 245	
ATC GGC GAC CGG TTC CAC GCG ATC CTG GTC GAC AAC GGT GTT CTG CGC	1241
Ile Gly Asp Arg Phe His Ala Ile Leu Val Asp Asn Gly Val Leu Arg	
250 255 260	
CTC AAC GAA GCG GCC AAT GTG AAG AAA ATC CTC GGC GAG GGC TTG GGC	1289
Leu Asn Glu Ala Ala Asn Val Lys Lys Ile Leu Gly Glu Gly Leu Gly	
265 270 275	
ATC AAC TTG ACT GTT GTT GAC GCC TCC GAA GAG TTC TTG ACG AAG CTC	1337
Ile Asn Leu Thr Val Val Asp Ala Ser Glu Glu Phe Leu Thr Lys Leu	
280 285 290	
AAG GGC GTC ACG GAC CCT GAG AAG AAG AGA AAG ATC ATC GGT AAC ACC	1385
Lys Gly Val Thr Asp Pro Glu Lys Lys Arg Lys Ile Ile Gly Asn Thr	
295 300 305 310	
TTC ATT CAT GTT TTT GAG CGC GAG GCA GCC AGG ATC CAG CCT AAG AAC	1433
Phe Ile His Val Phe Glu Arg Glu Ala Ala Arg Ile Gln Pro Lys Asn	
315 320 325	
GGC GAG GAG ATT GAG TTC CTG TTG CAG GGT ACC CTA TAC CCT GAC GTT	1481
Gly Glu Glu Ile Glu Phe Leu Leu Gln Gly Thr Leu Tyr Pro Asp Val	
330 335 340	
ATC GAG TCC ATT TCC TTT AAG GGC CCA TCT CAG ACG ATC AAG ACC CAC	1529
Ile Glu Ser Ile Ser Phe Lys Gly Pro Ser Gln Thr Ile Lys Thr His	
345 350 355	

10076457.024502

CAT AAC GTC GGT GGT CTT TTG GAC AAC ATG AAA CTG AAG CTC ATT GAG 1577  
 His Asn Val Gly Gly Leu Leu Asp Asn Met Lys Leu Lys Leu Ile Glu  
 360 365 370

CCT TTG CGC GAG CTT TTC AAG GAC GAG GTG AGA CAC CTG GGA GAA CTA 1625  
 Pro Leu Arg Glu Leu Phe Lys Asp Glu Val Arg His Leu Gly Glu Leu  
 375 380 385 390

TTG GGG ATC TCC CAC GAG TTG GTC TGG AGA CAT CCG TTC CCA GGC CCA 1673  
 Leu Gly Ile Ser His Glu Leu Val Trp Arg His Pro Phe Pro Gly Pro  
 395 400 405

GGT ATC GCC ATC CGT GTG CTA GGC GAG GTC ACC AAG GAG CAG GTG GAG 1721  
 Gly Ile Ala Ile Arg Val Leu Gly Glu Val Thr Lys Glu Gln Val Glu  
 410 415 420

ATT GCC AGA AAG GCA GAC CAC ATC TAC ATC GAG GAG ATC AGG AAA GCA 1769  
 Ile Ala Arg Lys Ala Asp His Ile Tyr Ile Glu Glu Ile Arg Lys Ala  
 425 430 435

GGT CTA TAC AAC AAG ATT TCT CAA GCT TTT GCT TGC TTG CTG CCT GTT 1817  
 Gly Leu Tyr Asn Lys Ile Ser Gln Ala Phe Ala Cys Leu Leu Pro Val  
 440 445 450

AAG TCT GTG GGT GTC ATG GGT GAC CAG AGA ACC TAC GAC CAG GTC ATT 1865  
 Lys Ser Val Gly Val Met Gly Asp Gln Arg Thr Tyr Asp Gln Val Ile  
 455 460 465 470

GCT CTA AGA GCA ATT GAG ACC ACG GAC TTC ATG ACT GCC GAC TGG TAT 1913  
 Ala Leu Arg Ala Ile Glu Thr Thr Asp Phe Met Thr Ala Asp Trp Tyr  
 475 480 485

CCA TTT GAG CAC GAA TTC TTG AAG CAT GTC GCA TCC CGT ATT GTT AAC 1961  
 Pro Phe Glu His Glu Phe Leu Lys His Val Ala Ser Arg Ile Val Asn  
 490 495 500

GAG GTT GAA GGT GTT GCC AGA GTC ACC TAC GAC ATA ACT TCT AAG CCT 2009  
 Glu Val Glu Gly Val Ala Arg Val Thr Tyr Asp Ile Thr Ser Lys Pro  
 505 510 515

CCA GCT ACC GTT GAA TGG GAA TAATCACCCT TGGGATCCGC TGA CTGGCTA 2060  
 Pro Ala Thr Val Glu Trp Glu  
 520 525

CTGTAATTCT ATGTAGTGA TTAGTACGAT AAGTTACTTT TGTATGATAG ATGTAATCAC 2120

ATCTGGCTAT TAAAATGACT CAGCCGAGGT AAATCTAACG TCCCTTCACA AGGGTGTTC 2180

TGTGTGGACT TCCGCCTGAA TTTTATAGA TATATAGATA CTCTACTCAT GAACAACCTG 2240

2007-12-15 10:24:00

CAACCGAATA AGCATTAGTG CCAGGAGAAG AGAACCGTGG AAATGGGGCA AGTAGAAAAA 2300  
 ATCATATTCC TTAAGAATAA GACAGTACCA GAGGACCATT ACGAGACGAT TTTTGAATCG 2360  
 AATGGCTTCC AGACTCACTT TGTACCCATA ATAACCCATG AACACCTGCC AGATGAGGTT 2420  
 CGCGGTCGAC TATCCGACGC GAATTACATG AAAAGGTTGA ATTGTTTGGT GGTAACCTCT 2480  
 CAGAGGACTG TGGAGTGTCT CTATGAGGAC GTTCTGCCCT CTCTTCCAGC TGAAGCACGC 2540  
 AAATCTCTTC TCAATACGCC AGTATTCGTG GTTGGGCGTG CCACTCAGGA ATTTATGGAG 2600  
 AGATGCGGCT TTACGGACGT GAGAGGGGGA TCTGAGACTG GTAATGGCGT TTTGCTAGCG 2660  
 GAGTTAATGT TAAATATGAT CCAGAAGGGC GATGGGG 2697

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met	Ala	Ala	Val	Glu	Gln	Val	Ser	Ser	Val	Phe	Asp	Thr	Ile	Leu	Val
1				5					10					15	
Leu	Asp	Phe	Gly	Ser	Gln	Tyr	Ser	His	Leu	Ile	Thr	Arg	Arg	Leu	Arg
			20					25					30		
Glu	Phe	Asn	Val	Tyr	Ala	Glu	Met	Leu	Pro	Cys	Thr	Gln	Lys	Ile	Ser
		35					40					45			
Glu	Leu	Gly	Trp	Lys	Pro	Lys	Gly	Val	Ile	Leu	Ser	Gly	Gly	Pro	Tyr
	50					55					60				
Ser	Val	Tyr	Ala	Ala	Asp	Ala	Pro	His	Val	Asp	Arg	Ala	Val	Phe	Glu
	65				70					75				80	
Leu	Gly	Val	Pro	Ile	Leu	Gly	Ile	Cys	Tyr	Gly	Leu	Gln	Glu	Leu	Ala
				85				90					95		
Trp	Ile	Ala	Gly	Ala	Glu	Val	Gly	Arg	Gly	Glu	Lys	Arg	Glu	Tyr	Gly
		100						105					110		



Arg Ala Thr Leu His Val Glu Asp Ser Ala Cys Pro Leu Phe Asn Asn  
 115 120 125  
 Val Asp Ser Ser Thr Val Trp Met Ser His Gly Asp Lys Leu His Ala  
 130 135 140  
 Leu Pro Ala Asp Phe His Val Thr Ala Thr Thr Glu Asn Ser Pro Phe  
 145 150 155 160  
 Cys Gly Ile Ala His Asp Ser Lys Pro Ile Phe Gly Ile Gln Phe His  
 165 170 175  
 Pro Glu Val Thr His Ser Ser Gln Gly Lys Thr Leu Leu Lys Asn Phe  
 180 185 190  
 Ala Val Glu Ile Cys Gln Ala Ala Gln Thr Trp Thr Met Glu Asn Phe  
 195 200 205  
 Ile Asp Thr Glu Ile Gln Arg Ile Arg Thr Leu Val Gly Pro Thr Ala  
 210 215 220  
 Glu Val Ile Gly Ala Val Ser Gly Gly Val Asp Ser Thr Val Ala Ala  
 225 230 235 240  
 Lys Leu Met Thr Glu Ala Ile Gly Asp Arg Phe His Ala Ile Leu Val  
 245 250 255  
 Asp Asn Gly Val Leu Arg Leu Asn Glu Ala Ala Asn Val Lys Lys Ile  
 260 265 270  
 Leu Gly Glu Gly Leu Gly Ile Asn Leu Thr Val Val Asp Ala Ser Glu  
 275 280 285  
 Glu Phe Leu Thr Lys Leu Lys Gly Val Thr Asp Pro Glu Lys Lys Arg  
 290 295 300  
 Lys Ile Ile Gly Asn Thr Phe Ile His Val Phe Glu Arg Glu Ala Ala  
 305 310 315 320  
 Arg Ile Gln Pro Lys Asn Gly Glu Glu Ile Glu Phe Leu Leu Gln Gly  
 325 330 335  
 Thr Leu Tyr Pro Asp Val Ile Glu Ser Ile Ser Phe Lys Gly Pro Ser  
 340 345 350  
 Gln Thr Ile Lys Thr His His Asn Val Gly Gly Leu Leu Asp Asn Met  
 355 360 365  
 Lys Leu Lys Leu Ile Glu Pro Leu Arg Glu Leu Phe Lys Asp Glu Val  
 370 375 380

10076157  
 001502

Arg His Leu Gly Glu Leu Leu Gly Ile Ser His Glu Leu Val Trp Arg  
 385 390 395 400  
 His Pro Phe Pro Gly Pro Gly Ile Ala Ile Arg Val Leu Gly Glu Val  
 405 410 415  
 Thr Lys Glu Gln Val Glu Ile Ala Arg Lys Ala Asp His Ile Tyr Ile  
 420 425 430  
 Glu Glu Ile Arg Lys Ala Gly Leu Tyr Asn Lys Ile Ser Gln Ala Phe  
 435 440 445  
 Ala Cys Leu Leu Pro Val Lys Ser Val Gly Val Met Gly Asp Gln Arg  
 450 455 460  
 Thr Tyr Asp Gln Val Ile Ala Leu Arg Ala Ile Glu Thr Thr Asp Phe  
 465 470 475 480  
 Met Thr Ala Asp Trp Tyr Pro Phe Glu His Glu Phe Leu Lys His Val  
 485 490 495  
 Ala Ser Arg Ile Val Asn Glu Val Glu Gly Val Ala Arg Val Thr Tyr  
 500 505 510  
 Asp Ile Thr Ser Lys Pro Pro Ala Thr Val Glu Trp Glu  
 515 520 525

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1634 Base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA for mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

## (ix) FEATURES:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..519

## (ix) FEATURES:

- (A) NAME/KEY: CDS

(ix) FEATURES:

(B) LOCATION: 1483..1634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCTCGAACAT CTATCTTCTG AGCTCGATAG TCTACGAAAT CGGCACACTA GCCTAATTGC	60
CGAGATGAAG AGCTCCAGGG AACCGTTAAA GATCTGATGT TCCATCTTCA ATCAGGACAA	120
ATGTTACGGG ATGTCCCTGA CGCCACAGAA GGTAGCCTGG TGGTCCAGAC AGAAAAAGAG	180
CCTACACCAA AGAAGAAACA TAACAAGAAA AAGCCTCCGC ATCGTTTTTG TAAATCATAA	240
TAGGCACGAT GCGCATATAC CCTGACCATC ATAGCGGTTC CCCCCGCTAA CTGCTCCGAG	300
CGGGTAACCC CATGTCACAA AGTGACTCTG TCTCTTCGTG GTAGGTGATG TCAAATTTTC	360
ACGACTTCCC ACCCCGATGA GCATCCGTAT TCCTTTTCAT CTAAATTCTA ATAGATGGCT	420
TATGGATTCT TATTGGCGAC TTACAAGCCT ATGTAGTTGG CTTCCCTCAA GTGTTCGTAG	480
TCTACCACCT CACACCCGGT CTAACAGCTT ACGAGAATA ATG GCT ACT AAT GCA	534
Met Ala Thr Asn Ala	
1 5	
ATC AAG CTT CTT GCG CCA GAT ATC CAC AGG GGT CTG GCA GAG CTG GTC	582
Ile Lys Leu Leu Ala Pro Asp Ile His Arg Gly Leu Ala Glu Leu Val	
10 15 20	
GCT AAA CGC CTA GGC TTA CGT CTG ACA GAC TGC AAG CTT AAG CGG GAT	630
Ala Lys Arg Leu Gly Leu Arg Leu Thr Asp Cys Lys Leu Lys Arg Asp	
25 30 35	
TGT AAC GGG GAG GCG ACA TTT TCG ATC GGA GAA TCT GTT CGA GAC CAG	678
Cys Asn Gly Glu Ala Thr Phe Ser Ile Gly Glu Ser Val Arg Asp Gln	
40 45 50	
GAT ATC TAC ATC ATC ACG CAG GTG GGG TCC GGG GAC GTG AAC GAC CGA	726
Asp Ile Tyr Ile Ile Thr Gln Val Gly Ser Gly Asp Val Asn Asp Arg	
55 60 65	
GTG CTG GAG CTG CTC ATC ATG ATC AAC GCT AGC AAG ACG GCG TCT GCG	774
Val Leu Glu Leu Leu Ile Met Ile Asn Ala Ser Lys Thr Ala Ser Ala	
70 75 80 85	
CGG CGA ATT ACG GCT GTG ATT CCA AAC TTC CCA TAC GCG CGG CAG GAC	822
Arg Arg Ile Thr Ala Val Ile Pro Asn Phe Pro Tyr Ala Arg Gln Asp	
90 95 100	

CGG AAG GAT AAG TCA CGG GCG CCA ATT ACC GCG AAG CTC ATG GCG GAC	870
Arg Lys Asp Lys Ser Arg Ala Pro Ile Thr Ala Lys Leu Met Ala Asp	
105 110 115	
ATG CTG ACT ACC GCG GGC TGC GAT CAT GTC ATC ACC ATG GAC TTA CAC	918
Met Leu Thr Thr Ala Gly Cys Asp His Val Ile Thr Met Asp Leu His	
120 125 130	
GCT TCG CAA ATC CAG GGC TTC TTT GAT GTA CCA GTT GAC AAC CTT TAC	966
Ala Ser Gln Ile Gln Gly Phe Phe Asp Val Pro Val Asp Asn Leu Tyr	
135 140 145	
GCA GAG CCT AGC GTG GTG AAG TAT ATC AAG GAG CAT ATT CCC CAC GAC	1014
Ala Glu Pro Ser Val Val Lys Tyr Ile Lys Glu His Ile Pro His Asp	
150 155 160 165	
GAT GCC ATC ATC ATC TCG CCG GAT GCT GGT GGT GCC AAA CGT GCG TCG	1062
Asp Ala Ile Ile Ile Ser Pro Asp Ala Gly Gly Ala Lys Arg Ala Ser	
170 175 180	
CTT CTA TCA GAT CGC CTA AAC TTG AAC TTT GCG CTG ATT CAT AAG GAA	1110
Leu Leu Ser Asp Arg Leu Asn Leu Asn Phe Ala Leu Ile His Lys Glu	
185 190 195	
CGT GCA AAG GCA AAC GAA GTG TCC CGC ATG GTT CTG GTC GGC GAT GTT	1158
Arg Ala Lys Ala Asn Glu Val Ser Arg Met Val Leu Val Gly Asp Val	
200 205 210	
ACC GAT AAA GTC TGC ATT ATC GTT GAC GAT ATG GCG GAT ACT TGT GGT	1206
Thr Asp Lys Val Cys Ile Ile Val Asp Asp Met Ala Asp Thr Cys Gly	
215 220 225	
ACG CTG GCC AAG GCG GCA GAA GTG CTG CTA GAG CAC AAC GCG CGG TCT	1254
Thr Leu Ala Lys Ala Ala Glu Val Leu Leu Glu His Asn Ala Arg Ser	
230 235 240 245	
GTG ATA GCC ATT GTT ACC CAC GGT ATC CTT TCA GGA AAG GCC ATT GAG	1302
Val Ile Ala Ile Val Thr His Gly Ile Leu Ser Gly Lys Ala Ile Glu	
250 255 260	
AAC ATC AAC AAT TCG AAG CTT GAT AGG GTT GTG TGT ACC AAC ACC GTG	1350
Asn Ile Asn Asn Ser Lys Leu Asp Arg Val Val Cys Thr Asn Thr Val	
265 270 275	
CCA TTC GAG GAG AAG ATG AAG TTA TGC CCG AAG TTA GAT GTA ATT GAT	1398
Pro Phe Glu Glu Lys Met Lys Leu Cys Pro Lys Leu Asp Val Ile Asp	
280 285 290	
ATC TCG GCA GTT CTT GCG GAA TCC ATT CGC CGT CTA CAC AAT GGT GAA	1446
Ile Ser Ala Val Leu Ala Glu Ser Ile Arg Arg Leu His Asn Gly Glu	
295 300 305	

AGT ATC TCC TAC CTC TTT AAA AAC AAC CCA CTA TGATTTTGCT TCTCGATGCT 1499  
 Ser Ile Ser Tyr Leu Phe Lys Asn Asn Pro Leu  
 310 315 320

GGCTTCTTGA GGGCCAATTT TGCCGTAGAG GTAGTATCCC TTCTTTTAT ATTGACTATT 1559  
 TAACGAAGAC TATTTCTTCA TAAATGGACT TCGGCTTCAC TGTGAATCTC ACATGATATA 1619  
 GTTGTTTCAG AGACC 1634

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Ala Thr Asn Ala Ile Lys Leu Leu Ala Pro Asp Ile His Arg Gly  
 1 5 10 15

Leu Ala Glu Leu Val Ala Lys Arg Leu Gly Leu Arg Leu Thr Asp Cys  
 20 25 30

Lys Leu Lys Arg Asp Cys Asn Gly Glu Ala Thr Phe Ser Ile Gly Glu  
 35 40 45

Ser Val Arg Asp Gln Asp Ile Tyr Ile Ile Thr Gln Val Gly Ser Gly  
 50 55 60

Asp Val Asn Asp Arg Val Leu Glu Leu Leu Ile Met Ile Asn Ala Ser  
 65 70 75 80

Lys Thr Ala Ser Ala Arg Arg Ile Thr Ala Val Ile Pro Asn Phe Pro  
 85 90 95

Tyr Ala Arg Gln Asp Arg Lys Asp Lys Ser Arg Ala Pro Ile Thr Ala  
 100 105 110

Lys Leu Met Ala Asp Met Leu Thr Thr Ala Gly Cys Asp His Val Ile  
 115 120 125

Thr Met Asp Leu His Ala Ser Gln Ile Gln Gly Phe Phe Asp Val Pro  
 130 135 140

Val Asp Asn Leu Tyr Ala Glu Pro Ser Val Val Lys Tyr Ile Lys Glu  
 145 150 155 160

His Ile Pro His Asp Asp Ala Ile Ile Ile Ser Pro Asp Ala Gly Gly  
 165 170 175

10076457.021502

Ala Lys Arg	Ala Ser Leu Leu Ser	Asp Arg Leu Asn Leu Asn Phe Ala
180	185	190
Leu Ile His Lys Glu Arg	Ala Lys Ala Asn Glu Val Ser Arg Met Val	
195	200	205
Leu Val Gly Asp Val Thr Asp Lys Val Cys Ile Ile Val Asp Asp Met		
210	215	220
Ala Asp Thr Cys Gly Thr Leu Ala Lys Ala Ala Glu Val Leu Leu Glu		
225	230	235 240
His Asn Ala Arg Ser Val Ile Ala Ile Val Thr His Gly Ile Leu Ser		
245	250	255
Gly Lys Ala Ile Glu Asn Ile Asn Asn Ser Lys Leu Asp Arg Val Val		
260	265	270
Cys Thr Asn Thr Val Pro Phe Glu Glu Lys Met Lys Leu Cys Pro Lys		
275	280	285
Leu Asp Val Ile Asp Ile Ser Ala Val Leu Ala Glu Ser Ile Arg Arg		
290	295	300
Leu His Asn Gly Glu Ser Ile Ser Tyr Leu Phe Lys Asn Asn Pro Leu		
305	310	315 320

20576457-021502